

STIC-Biotech/ChemLib

175467

From: Chernyshev, Olga
Sent: Tuesday, January 03, 2006 1:02 PM
To: STIC-Biotech/ChemLib
Subject: 09/869,486; sequence search request

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JAN - 3 2006
STIC-BIOTECH/CHEN, O.
(STIC)

US case 09/869,486

Please search SEQ ID NO: 25, 29 and 30, and fragment 73-3714 of SEQ ID NO: 29 in regular and pending databases.

Thank you very much!

Olga N. Chernyshev, Ph.D.

AU 1649

REM 3C89

2-0870

mail 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Db 314 TVYDFEGEGSEBELDTYIKALVKACKSHSQEPQYUDELKLAIVAMDRVDIAKSEIFNGDV 373
Qy 419 QMSFHLBASLMDALLNDREPEFVRLISGSLSGHFTTPMRLAQLYSAASNSLIRLTD 478
Db 374 EWSKCDLEBVMVALVSNKPEFVRLFDNGADVADFTYGLQELVYSVRKSLFLPDLQ 433
Qy 479 QASHSAGTKAPALKGAAELRPP-----DVGVLRLMLGKMKCAPYPSGAMP 528
Db 434 RKOBEARLTLAGL--GTQARPEPPAGPPAPSIHVSRLVDPLQDACKGYQDGRPDGR 491
Qy 529 -----PGQGFESMYLLSDKATSPSLDAGLQAPMSDLLMALINRAQMANFWMG 583
Db 492 RAEKGPAPKPTQGMCLDLNOKS-----ENPMRDLFLMAYLQHRHEMATYFAMGQ 542
Qy 584 NAVSALGACLLLRVMALEPDAEBAARRDLAKFEGMGVDFGECYSSVPAAALL 643
Db 543 EGVAAALAAKCKIKEMSHLETBAARAATREA--KYBQLALDLFSECYSSSEAAAFALLV 600
Qy 644 RRCPLMGDATCLOLAMOADAAPPAODGVOSLITOKMGDMASSTPIWALVAFPCPLI 703
Db 601 RRRRCHSKTCLHATBDADAKAPFAHDGVAFLTRIMGDMAGTPIRLILGAFCLALV 660
Qy 704 YTRLITFRKSEBETREBEL--FDMDSVINGEGVGTADPAEKTPLGVPPOSGRPGCCG 761
Db 661 YTNLITF--SEBAPLRTGLBDLODLSLDTEKSPLYGLQSRVBEVLEAPRAQGD----- 742
Qy 762 RCGGRRC--LRWFHFWGAPVTITFMGNVSYLLFLILFSRVLLVNDQAP--PGSLLEL 816
Db 713 --RGPRAVFLTLTRKRWGAPVTITFGNVVYPAFLFTYVLLVNDPRPPOSGSGEVT 770
Qy 817 LYFMAFLICEBLROGSLGGGSLASGPGGHASLSORLRYLADSMNOCDDVALTCFL 876
Db 771 LYFMAFLICEBLROGSPFTBEDT-----HLVKETLYVGDMMKCDVAILFLPI 819
Qy 877 LGVGCRLTPGLYHIGRTVLCIDFMVFTVRLLIHFTVVKOLGPKIVISKMKOVFFFLPF 936
Db 820 VGVTCKMLPSAPFAGRTVLAADFVFTVRLIHFPAIKHQLGPKIIVERAMKOVFFFLPF 879
Qy 937 LGSVWLVAAGVATGELLRPRSDPPSILRRVTPRYLOIFQOIQEDMDVALMHSNCSSE 936
Db 880 LSWWLVAAGVATGELLRPRSDPPSILRRVTPRYLOIFQOIQEDMDVALMHSNCSSE 936
Qy 997 PGFMAHPGAQAGTCVSOYANMLVLLVFLVLANILVNLILAMPSTYFGKVGQNSDL 1056
Db 937 PLLLEBSP-----SCPSLYANMLVILLVFLVLANILVNLILAMPSTYFGVQNSADM 991
Qy 1057 YWKAQRYRLIRBPHSPALAPPTIVISHLRLRLQLCRPPSPQSSPALHFRVYLSKE 1116
Db 992 FMKFORYNLIVEYHERPALAPPTILSHLSLTLARVFK-----BAHKKREHLERD 1042
Qy 1117 ----ABKLLTWESYKHNENFLIARADKESDSRLKRTOKUDLAKOIGHIRYQRL 1172
Db 1043 LPPDLQKVTWETVOENFLSKMEKRRRDSBEGVLEKTAHRVDPLAKYLGGIAREDEKRI 1102
Qy 1173 KVLREYVOQSRVYGVAEALSREALLPPOGP 1204
Db 1103 KCLSEQINYSVSVSVADVLAQ-----GSP 1129

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RESULT 2
US-09-949-016-6874
Sequence 6874, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 6874
; LENGTH: 1165
; TYPE: PRN
; ORGANISM: Human
US-09-949-016-6874
Query Match 38.4%; Score 2448.5; DB 2; Length 1165;
Best Local Similarity 45.6%; Pred. No. 1.6e-223;
Matches 534; Conservative 177; Mismatches 350; Indels 11; Gaps 26;

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Qy 76 GELDPTGAGKHSNPLRLSRTDPAVYSLVITWTGGRANLYVSVGSGGFPVLTQ 135
Db 26 GEVNFSGGKRRKFPVPSGVAPSVLFDLLLEWMLPAENLVSVLVBEGQPPAMKSMIR 85
Qy 136 DLRRGLVRAAGSTGAMIVTGLHTGIGRHVAVVRDHOMASTG-GTKVAMGVAPWGVV 194
Db 86 DVLRKGLVKAAGSTGAMILTSALRVGLARVGOAVRDHSLASTSTKRVVAVGMAISGRV 145
Qy 195 RNRDTLINPGSPAPRYRWGDEPD--GVQFP--IDYNSAFELVDGTHGCLGGENRF 249
Db 146 LHRRIIEBAQEDPPVHY-----PEDDGGSGPLCSIDSNLSHFTLVBPGRKGDGLTEL 200
Qy 250 RLRLSEYISQKTKVGSTG-IDIPVLLILIDGEBKLTREANATQALPCLLVAGSGGA 308
Db 201 RLRLKHIISQRAQYGGTGISIRPVLCLVMDPNTLERSRVEQAAPWLILVSGGIA 260
Qy 309 DCLAETLED--TLAPSGAGQGBARDRIKPPPK-----GDLEVLQAVERTREKEL 361
Db 261 DVLAALVNOPHLV-----KVAEKQFKEKPSKFSMEDVVRTKYLQNTSHQHL 313
Qy 362 TVYSSE-DGSEBEFETIVLKAIVAC--GSGSASAYLDELRLAAMNRVDIAQSELFRDI 418
Db 314 TVYDFEGEGSEBELDTYIKALVKACKSHSQEPQYUDELKLAIVAMDRVDIAKSEIFNGDV 373
Qy 419 QMSFHLBASLMDALLNDREPEFVRLISGSLSGHFTTPMRLAQLYSAASNSLIRLTD 478
Db 374 EWSKCDLEBVMVALVSNKPEFVRLFDNGADVADFTYGLQELVYSVRKSLFLPDLQ 433
Qy 479 QASHSAGTKAPALKGAAELRPP-----DVGVLRLMLGKMKCAPYPSGAMP 528
Db 434 RKOBEARLTLAGL--GTQARPEPPAGPPAPSIHVSRLVDPLQDACKGYQDGRPDGR 491
Qy 529 -----PGQGFESMYLLSDKATSPSLDAGLQAPMSDLLMALINRAQMANFWMG 583
Db 492 RAEKGPAPKPTQGMCLDLNOKS-----ENPMRDLFLMAYLQHRHEMATYFAMGQ 542
Qy 584 NAVSALGACLLLRVMALEPDAEBAARRDLAKFEGMGVDFGECYSSVPAAALL 643
Db 543 EGVAAALAAKCKIKEMSHLETBAARAATREA--KYERLALDLFSECYSSSEAAAFALLV 600
Qy 644 RRCPLMGDATCLOLAMOADAAPPAODGVOSLITOKMGDMASSTPIWALVAFPCPLI 703
Db 601 RRRRCHSKTCLHATBDADAKAPFAHDGVAFLTRIMGDMAGTPIRLILGAFCLALV 660
Qy 704 YTRLITFRKSEBETREBEL--FDMDSVINGEGVGTADPAEKTPLGVPPOSGRPGCCG 761
Db 661 YTNLITF--SEBAPLRTGLBDLODLSLDTEKSPLYGLQSRVBEVLEAPRAQGD----- 742
Qy 762 RCGGRRC--LRWFHFWGAPVTITFMGNVSYLLFLILFSRVLLVNDQAP--PGSLLEL 816
Db 713 --RGPRAVFLTLTRKRWGAPVTITFGNVVYPAFLFTYVLLVNDPRPPOSGSGEVT 770
Qy 817 LYFMAFLICEBLROGSLGGGSLASGPGGHASLSORLRYLADSMNOCDDVALTCFL 876
Db 771 LYFMAFLICEBLROGSPFTBEDT-----HLVKETLYVGDMMKCDVAILFLPI 819
Qy 877 LGVGCRLTPGLYHIGRTVLCIDFMVFTVRLLIHFTVVKOLGPKIVISKMKOVFFFLPF 936

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 08:55:52 ; Search time 171 Seconds

(without alignments)
5008.838 Million cell updates/sec

Title: US-09-869-486b-30

Sequence: 1 MVEPKRQSWIPKIPKKTCTC.....RSALPPGPPPDLPGRKD 1214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_09_80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6383	100.0	1214	2	Q8TD43 HUMAN
2	5505.5	86.3	1069	2	Q7ZSD9 HUMAN
3	5454	85.4	1040	2	Q96184 HUMAN
4	5316	83.3	1016	2	Q9NXY1 HUMAN
5	5194.5	81.4	1213	2	Q7TN37 MOUSE
6	4001.5	62.7	945	2	Q8BLM7 MOUSE
7	3564	55.8	872	2	Q6PDM0 MOUSE
8	3375	52.9	686	2	Q8HXH2 MACRA
9	3189	50.0	799	2	Q80194 MOUSE
10	2452.5	38.4	1165	2	Q52LU2 HUMAN
11	2448.5	38.4	1165	2	Q9NZ08 HUMAN
12	2437.5	38.2	1159	2	Q9NY34 HUMAN
13	2397.5	37.6	1158	2	Q9BPM4 MOUSE
14	2397.5	37.6	1158	2	Q9LJH7 MOUSE
15	2396.5	37.5	1148	2	Q9NRP9 MOUSE
16	2376.5	37.2	1116	2	Q9BPM3 MOUSE
17	2310.5	36.2	1297	2	Q4RYK8 TETNG
18	2088	32.7	1030	2	Q8BS44 MOUSE
19	2050.5	32.1	510	2	Q80Y33 MOUSE
20	2048.5	32.1	1000	2	Q7TPI4 MOUSE
21	2011.5	31.5	779	2	Q7TOM9 XENLA
22	2000	31.5	485	2	Q9BS05 RAT
23	1961.5	30.7	1488	2	Q769E2 MOUSE
24	1945	30.5	1503	1	TRPM2 HUMAN
25	1945	30.5	1503	2	Q5KTC2 HUMAN
26	1896.5	29.7	1507	1	TRPM2 MOUSE
27	1894	29.7	1506	2	Q5KTC0 MOUSE
28	1886.5	28.6	1508	2	Q5G8E6 RAT
29	1813.5	25.8	803	2	Q4SHZ2 TETNG
30	1646.5	25.8	1095	2	Q5UKZ3 CHICK
31	1625.5	25.5	422	2	Q769E4 MOUSE

32	1612.5	25.3	1104	1	TRPM8 RAT	Q8r455	rattus norv
33	1608.5	25.2	1104	1	TRPM8 HUMAN	Q7z227	homo sapien
34	1606.5	25.2	1224	2	Q4RQPS TETNG	Q4RQPS	tetraodon n
35	1604	25.1	1289	1	Q5KTC1 HUMAN	Q5KTC1	homo sapien
36	1597.5	25.0	1104	2	TRPM8 MOUSE	Q8r4d5	mus musc
37	1622.5	22.9	567	2	Q6GPZ7 XENLA	Q6GPZ7	xenopus lae
38	1435	22.5	1709	2	Q5F4S7 MOUSE	Q5F4S7	mus musc
39	1435	22.5	1718	2	Q69ZB8 MOUSE	Q69ZB8	mus musc
40	1433.5	22.5	1732	1	TRPM3 HUMAN	Q9hcf6	homo sapien
41	1432	22.4	1721	2	Q5F4S9 MOUSE	Q5F4S9	mus musc
42	1432	22.4	1721	2	Q5F4T0 MOUSE	Q5F4T0	mus musc
43	1430.5	22.4	340	2	Q811B2 MOUSE	Q811B2	mus musc
44	1429	22.4	1699	2	Q5F4S6 MOUSE	Q5F4S6	mus musc
45	1426	22.3	1711	2	Q5F4S8 MOUSE	Q5F4S8	mus musc

ALIGNMENTS

RESULT 1
Q8TD43 HUMAN PRELIMINARY; PRT; 1214 AA.
ID Q8TD43 HUMAN
AC Q8TD43
DT 01-JUN-2002 (TRMBLrel. 21, Created)
DT 01-JUN-2002 (TRMBLrel. 21, Last sequence update)
DT 01-FEB-2005 (TRMBLrel. 29, Last annotation update)
DE Cation channel TRPM4B (Transient receptor potential ion channel
DE melastatin subgroup member 4 protein) (Transient receptor potential
DE cation channel subfamily M member 4 splice variant B).
GN Name=TRPM4; Synonyms=TRPM4B;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini; Homidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22011788; PubMed=12015988; DOI=10.1016/S0092-8674(02)00719-5;
RA Launay P., Fleig A., Peraldo A.L., Scharenberg A.M., Penner R.,
RA Kinet J.P., Ca2+-activated nonselective cation channel mediating cell
RT "TRPM4 is a Ca2+-activated nonselective cation channel mediating cell
RL Cell 109:397-407(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Peraldo A.L., Scharenberg A.,
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200;
RA Nilius B., Pohlen J., Droogmans G., Voets T., Vennekens R.,
RA Freichel M., Wissenbach U., Flockerzi V.,
RL "Voltage dependence of the Ca2+-activated cation channel TRPM4.";
RL J. Biol. Chem. 278:30813-30820(2003).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2276392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubandov V., Gudermann T., Montell C.,
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent
RT selective cation channel.";
RL Curr. Biol. 13:1153-1158(2003).
EMBL: AF497623; AM18083.1; -; mRNA.
EMBL: AF575813; CA05941.1; -; mRNA.
EMBL: AF297045; AAP4474.1; -; mRNA.
DR Ensembl; ENSG00000130529; Homo sapiens.
DR HGNC; HGNC:17993; TRPM4.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat_channel_TipL.
DR InterPro; IPR005821; Ion_trans.

DR Pfam; PF00520; Ion_chan; 1.
KW Receptor.
SQ SEQUENCE 1214 AA; 134300 MW; 76ADA45269BD8F5 CRC64;
Query Match 100.0%; Score 6393; DB 2; Length 1214;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPVEKQSWI PKI FKKKCTTFFIVDSTDPGTLCCGGRPTAHPAVAMEDAGAAVTV 60
DB 1 MNPVEKQSWI PKI FKKKCTTFFIVDSTDPGTLCCGGRPTAHPAVAMEDAGAAVTV 60
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DB 61 WDSDAHTTEKPTDAYGELDTGAGRKHSNFTLSDRTPDAAYSLVTRTWGFRAPNLVVS 120
QY 121 VLGGSGGSPVLQTMQLDRLRGILVRAAOSTGAMITVGGILHTGIRHGVAVRDHOMASTGG 180
DB 121 VLGGSGGSPVLQTMQLDRLRGILVRAAOSTGAMITVGGILHTGIRHGVAVRDHOMASTGG 180
QY 181 TKVAVMGVAPWGVNRNDTLINPKGSPPARYRWGDEPDGVQPLDYNYSAPFLVDDGTH 240
DB 181 TKVAVMGVAPWGVNRNDTLINPKGSPPARYRWGDEPDGVQPLDYNYSAPFLVDDGTH 240
QY 241 GCLGGENRFLRLBSYISQOKTGVGIGTIDIPVLLLLIDDEKMLTRIENATOALPCLL 300
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DB 301 VAGSGGADCLATLREPTLA PGSGGARQGBARDIRFPFKGDLVLAQOVERIMTRKEL 360
QY 361 LTVYSSBDGSEEFETIVLKALVRCSSSEASAYLDELRLAVANRVYDIAOSELFRGDIOW 420
DB 361 LTVYSSBDGSEEFETIVLKALVRCSSSEASAYLDELRLAVANRVYDIAOSELFRGDIOW 420
QY 421 RSFHLBASLMDALLNRPBEVRLILSHGSLGHFLTPMRLAQLYSAFNSLIRNLLDOA 480
DB 421 RSFHLBASLMDALLNRPBEVRLILSHGSLGHFLTPMRLAQLYSAFNSLIRNLLDOA 480
QY 481 SHSAGTKAPLKGGAELRPDVGHVRLMLGKMKCAPRYSGGAMDHPQGGESWYLL 540
DB 481 SHSAGTKAPLKGGAELRPDVGHVRLMLGKMKCAPRYSGGAMDHPQGGESWYLL 540
QY 541 SDRATPLSLDAGIGAPMSDLLIMALLNRAQAMTFWEMGSNAVSALGACILLRYVA 600
DB 541 SDRATPLSLDAGIGAPMSDLLIMALLNRAQAMTFWEMGSNAVSALGACILLRYVA 600
QY 601 RLEPDABEAAARRKDLAFKFGMGVDLFGECYRSSSEVAARLLRRCPLMGDATCLOLMO 660
DB 601 RLEPDABEAAARRKDLAFKFGMGVDLFGECYRSSSEVAARLLRRCPLMGDATCLOLMO 660
QY 661 ADARAPPAODGVSLLTOKWGMMASTTPIWALVLAFCGPLLYTLITFRKSEBPTRE 720
DB 661 ADARAPPAODGVSLLTOKWGMMASTTPIWALVLAFCGPLLYTLITFRKSEBPTRE 720
QY 721 ELEFDMDSVINGEPVGTADPAEKTPLGVROSGRPCCGRCGRRCILRWHFHGAAY 780
DB 721 ELEFDMDSVINGEPVGTADPAEKTPLGVROSGRPCCGRCGRRCILRWHFHGAAY 780
QY 781 TTFMGVNVSTYLLALLPSRVLLVDFOAPAPPGSTLELLLYFMAFTLLCBEIRLQGLSGGGSL 840
DB 781 TTFMGVNVSTYLLALLPSRVLLVDFOAPAPPGSTLELLLYFMAFTLLCBEIRLQGLSGGGSL 840
QY 841 ASGGPBGHASTLSORLRLYADSNOCODVALTCPLLGVCRLTPGLYHNGRVLCTIDPM 900
DB 841 ASGGPBGHASTLSORLRLYADSNOCODVALTCPLLGVCRLTPGLYHNGRVLCTIDPM 900
QY 901 VFTVRLHLHFTVVKOLGPKIVISKMKOVFFFLFLGVLVAVGATGELLRPRSDPP 960
DB 901 VFTVRLHLHFTVVKOLGPKIVISKMKOVFFFLFLGVLVAVGATGELLRPRSDPP 960
QY 961 SLIRRVYRBYLQIFQOIQEDMDVALMEHSNCSSEBGFMAHPGAQACTCVSOYANMLV 1020

DB 961 SLIRRVYRBYLQIFQOIQEDMDVALMEHSNCSSEBGFMAHPGAQACTCVSOYANMLV 1020
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DB 1021 VLLLVFLVANILLVNLILAMFSYFGKVGQSDLYMKARVRLIREFHSRPAALPFI 1080
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DB 1081 VISHLRLRLQLCRPRSPQSSPALEHFRVYLSKAEERKLLTWESVHKENFLAARDK 1140
QY 1141 RESDSRLKRTSQKDLAKQUGHIREYBORLKYVERVQCGSRVYGVAEALSRBALP 1200
DB 1141 RESDSRLKRTSQKDLAKQUGHIREYBORLKYVERVQCGSRVYGVAEALSRBALP 1200
QY 1201 PGAPPPDLPGSKD 1214
DB 1201 PGAPPPDLPGSKD 1214
RESULT 2
Q7ZSD9 HUMAN
ID Q7ZSD9_HUMAN PRELIMINARY; PRT; 1069 AA.
AC Q7ZSD9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transient receptor potential cation channel subfamily M member 4
DE splice variant C.
GN Name=TRPM4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent
selective cation channel."
RL Curr. Biol. 13:1153-1156(2003).
EMBL: AY297046; AAB44475.1; -; mRNA.
DR Ensembl: ENSG00000130529; Homo sapiens.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:004872; F:receptor activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR002111; Cat_channel_TprL.
KW Receptor.
SQ SEQUENCE 1069 AA; 118629 MW; 80DEBD935A55F200 CRC64;
Query Match 86.3%; Score 5505.5; DB 2; Length 1069;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 0; Indels 145; Gaps 1;
QY 1 MNPVEKQSWI PKI FKKKCTTFFIVDSTDPGTLCCGGRPTAHPAVAMEDAGAAVTV 60
DB 1 MNPVEKQSWI PKI FKKKCTTFFIVDSTDPGTLCCGGRPTAHPAVAMEDAGAAVTV 60
QY 61 WDSDAHTTEKPTDAYGELDTGAGRKHSNFTLSDRTPDAAYSLVTRTWGFRAPNLVVS 120
DB 61 WDSDAHTTEKPTDAYGELDTGAGRKHSNFTLSDRTPDAAYSLVTRTWGFRAPNLVVS 120
QY 121 VLGGSGGSPVLQTMQLDRLRGILVRAAOSTGAMITVGGILHTGIRHGVAVRDHOMASTGG 180
DB 121 VLGGSGGSPVLQTMQLDRLRGILVRAAOSTGAMITVGGILHTGIRHGVAVRDHOMASTGG 180
QY 181 TKVAVMGVAPWGVNRNDTLINPKGSPPARYRWGDEPDGVQPLDYNYSAPFLVDDGTH 240
DB 181 TKVAVMGVAPWGVNRNDTLINPKGSPPARYRWGDEPDGVQPLDYNYSAPFLVDDGTH 240
QY 241 GCLGGENRFLRLBSYISQOKTGVGIGTIDIPVLLLLIDDEKMLTRIENATOALPCLL 300

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OM protein - protein search, using SW model

Run on: January 6, 2006, 08:55:56 : Search time 43 seconds
(without alignments) 2716.445 Million cell updates/sec

Title: US-09-869-486b-30

Perfect score: 6383
Sequence: 1 MVVPEKGGWIPKIFKKKTC.....RSALPFGGPPDLPSSKD 1214

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

1: PIR 80: *
2: PIR 1: *
3: PIR 2: *
4: PIR 3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1961.5	30.7	488	UC7995	transient receptor
2	1195.5	18.7	1868	T23707	hypothetical prote
3	1191.5	18.0	1400	T22644	hypothetical prote
4	1021.5	16.0	1707	T18951	hypothetical prote
5	248	3.9	899	P88391	protein R06810.4 (
6	247.5	3.9	1275	JU0092	trp protein - fru
7	246	3.9	1418	J40764	hypothetical prote
8	242	3.8	1274	JN0015	trp protein - fru
9	221.5	3.5	1124	JH0588	calmodulin-binding
10	209.5	3.3	823	S44873	zc21.2 protein - C
11	169	2.6	793	S68238	trp-1 protein - hu
12	169	2.6	810	T38361	TRPC1 protein - hu
13	167	2.6	828	JCS887	trp3 protein - rat
14	156	2.4	823	T34472	hypothetical prote
15	142.5	2.2	3413	T17467	riifamycin polypept
16	136	2.1	839	JC7661	capsaicin receptor
17	133	2.1	675	T20822	hypothetical prote
18	132	2.1	456	H84278	hypothetical prote
19	128	2.0	245	AH2002	hypothetical prote
20	127	2.0	1245	E83110	exodeoxyribonuclea
21	125	2.0	509	E83442	probable 3-hydroxy
22	125	2.0	1255	T31065	diaphanous protein
23	123	1.9	5069	T17464	riifamycin polypept
24	119	1.9	542	T28688	hypothetical prote
25	118.5	1.9	790	T20312	hypothetical prote
26	118	1.8	970	E70533	probable sulfatase
27	118	1.8	2222	A37490	voltage-dependent
28	118	1.8	2272	C54972	polyketide synthase
29	117.5	1.8	3739	T17410	

30	117.5	1.8	7463	2	T36248	CDA peptide synthe
31	116.5	1.8	727	2	UC7796	epithelial calcium
32	116.5	1.8	1076	2	C70749	probable ppa prot
33	116.5	1.8	7576	2	T17428	FK506 polypeptide s
34	116	1.8	765	2	H70763	probable glycy prot
35	116	1.8	900	2	T33026	hypothetical prote
36	116	1.8	1997	2	T30874	virginiamycin S by
37	116	1.8	2178	2	S29237	calcium channel pr
38	116	1.8	2259	2	S29236	calcium channel pr
39	115.5	1.8	838	2	T09054	capsaicin receptor
40	115.5	1.8	1438	2	T17402	dihydroerginone
41	115.5	1.8	1728	2	T17466	riifamycin polypept
42	115	1.8	598	2	B75626	PTS system, fructo
43	115	1.8	881	2	T03461	methyl-accepting c
44	114.5	1.8	735	2	T35778	probable fusidic a
45	114.5	1.8	854	2	T23155	hypothetical prote

ALIGNMENTS

RESULT 1

UC7995
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C:Accession: UC7995

R:Murakami, M.; Xu, F.; Miyoshi, I.; Sato, B.; Ono, K.; Iijima, T.

Biochem. Biophys. Res. Commun. 307, 522-528, 2003

A:Title: Identification and characterization of the murine TRPM4 channel.

A:Reference number: UC7995; PMID:12893253

A:Accession: UC7995

A:Molecule type: DNA

A:Residues: 1488 <MUR>

A:Cross-references: GB:NM000319

A:Experimental source: Brain, C57/BL6

A:Comment: This protein, a member of subfamily of transient receptor potential channels,

A:Gene: trpm4

A:Map position: 7B2

A:Intons: 12/2, 153/2, 197/3, 256/1, 315/2, 384/1, 428/2, 452/3

C:Keywords: calcium entry; transient receptor potential; transmembrane domain; TRPM

Query Match	30.7%	Score 1961.5	DB 2	Length 488
Best Local Similarity	77.6%	Pred. No. 3.5e-140		
Matches 384	Conservative 32	Mismatches 66	Indels 13	Gaps 5
QY	726	MDSVINGEGVGTADPAKKTPLGVPRQSGPG---CCGRCGGRCLRMFWGAPVTI	782	
DB	1	MDSINAGPGPTVPEPAKVAL-ERRQRAPGRALCCG-----KFSKMSDFGAPVTA	53	
QY	783	FMGNVSYLLFLFLFSVLLVDFOAPRPGSLLELLIYMAATTLCELRQSLGGGSLAS	842	
DB	54	FLGNVSYLLFLFLFAVLLVDFQPTPSVSELLIYMAATTLCELRQSLGGGSLAS	113	
QY	843	GGPGPGHASSORLRLYLADSMNOCDLVATCFLLGVGCLTPRLYHIGRTVLCIDPMVF	902	
DB	114	GGKGPDRAPLRRLHLYLSTMNOCDLATCFLLGVGCLTPRLFLGRTVLCIDPMIF	173	
QY	903	TVRLHILFTVNKOLGPRIVISRMKDVFFFLFGVWLVAAYGVATGGLLRPRSDPSPI	962	
DB	174	TVRLHILFTVNKOLGPRIVISRMKDVFFFLFGVWLVAAYGVATGGLLRPRSDPSPI	233	
QY	963	LRRVFRPYQIQGQIQGEMDVALMHSHSCSSRPGFWAPRPAQAQTCVQVNMIVL	1022	
DB	234	LRRVFRPYQIQGQIQGEMDVALMHSHSCSSRPGFWAPRPAQAQTCVQVNMIVL	293	
QY	1023	LIVFLVAVITLVNLLIAFSTYFGKVSNDLYWFAQRYRLIRFHSRPAAPPIVI	1082	
DB	294	LIVFLVAVITLVNLLIAFSTYFGKVSNDLYWFAQRYRLIRFHSRPAAPPIIII	353	
QY	1083	SHRLRLRLQ--CNR-PRSDPSPALRFRVYLKSKERKLTWESVHKENFLAADRD	1139	

Db 354 SHVRLIKWLRRRCRRANLPA5PVEHFRVCL5KEAKRLTWESVHKENFLLAQARD 413
QY 1140 KRESDESRLKRTSQKVDLALKOLGHIREFYORLKVLEREYQOCSRVLGVAALSSALL 1199
Db 414 KRSDSRLKRTSQKVDLALKOLGHIREFYORLKVLEREYQOCSRVLTWABALSSALL 473
QY 1200 PEGGPPPPDLPGSKD 1214
Db 474 PEGAPPPPPPTGSKD 488
RESULT 2
T23707
hypothetical protein T01H8.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_rev15ion 15-Oct-1999 #text_change 29-Oct-1999
C/Accession: T23707, T24342
R/Kerhaw, J.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19786
A/Accession: T23707
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 11868 <MIL>
A/Cross-references: UNIPARC:UPI000017BB41; EMBL:Z83117; PIDN:CAB05572.1; GSPDB:GN00019;
A/Experimental source: clone M04C7
R/Lemard, N.
submitted to the EMBL Data Library, September 1996
A/Reference number: Z19877
A/Accession: T24342
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1868 <M12>
A/Cross-references: UNIPARC:UPI000017BB41; EMBL:Z80219; PIDN:CAB02303.1; GSPDB:GN00019;
A/Experimental source: clone T01H8
C/Genetics:
A/Genes: CESP:T01H8.5
A/Map position: 1
A/Intons: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1
Query Match 18.7%; Score 1195.5; DB 2; Length 1868;
Best Local Similarity 24.8%; Pred. No. 2e-81;
Matches 385; Conservative 233; Mismatches 499; Indels 431; Gaps 51;
QY 9 SWIPKIFKKKCTCTTPTVSDTPGGTLCCGCRPRTAH-----PAVAMEDAF 53
Db 118 NWREFTREGRFASRD--HKCGGRTDAHNIPELTSBFLQKRSVALAQOR 175
QY 54 GAANVT-----VWSDAHTTEKPTDAYGELDTTGAGRKH-SNPLRLSDR 96
Db 176 SGNVNDINTOMMYTKRGANKEMKSLRKHTVSLATNAFGQVEFGGPHPYKAQYVRNP 235
QY 97 TDAAYVSVLTRYTWGPAPVLLVSVLGSGGSPVLQTMLODLRRGLVRAQSGAMVTVG 156
Db 236 TBAAYMSLEHAWQJSPRLIITVHGGSNFDLPRLARVFKGLKALASTIGAMITIS 255
QY 157 GLHTGIGRHGVAVNRDHQMASTGGTKVAVGAVPWGVNRDPLINPKGSFP-----ARY 211
Db 296 GCGTGVVGVAAALLEGASQNR--NKIVCIGIAPWGLTKGKEDFIQGDKVPVYPSSSKG 353
QY 212 RWRGDEPDGVQPLVDVYSAFPLVDDGTHGCLGGRNFRLLRLSYISQKTVGGTGIDI 271
Db 354 RFTG-----LNNHSYFLLVDNGTVGRYGAELVLRKLEMYISQKQIFGGTR-SV 403
QY 272 PVLLLLIDGD-----EKMLTIEANATQAOLPCLLVAGSGAADCLA-----ETLEDTLAPGS 323
Db 404 PVVCVAVLEGSSCTIRSVLDVYTVN--PRVAVVAVCDGSGRADLLAPAHQNTVEDGLP-- 459
QY 324 GGARQGEARDIRIRFPFGDLVYL-----QKQVERIM-----TRKELLTVYS- 365
Db 460 -----DDIR-----QVLLVETTFPGCSBAARHLHLBELVTCQAKHKLTLITFRL 503
QY 366 SEDGSEEFETTVLKALVYKACSSBAAYLDELRLAVANRVDIAQSELFGDITQMRSPHL 425

Db 504 GEQGEHDVHALITLALKQNTLSA-----DQLALALAMNRVDIARSDVFMGEHWQAL 559
QY 426 EASLADALINDREPRFRLIISHGLSLGFLTPRLALQIYSA--APNSILRLINDQASHS 483
Db 560 HNAEMELIHDRVDPRLLLEQGINNOKFLTISRLELVNTDGPENTLEFYIRDVVRVR 619
QY 484 AGTKAPALKGAAELRPPVGHVLRMLGKMCAPRY----- 519
Db 620 QGYR-----FLPDIGLVIETKMGNSYQCSYTSSEFRDKYQRMKRVGHAQKAM 669
QY 520 -----PS-----GGA-----WDPRP----- 529
Db 670 GVFSRRPSTGSGIASRQSTEGKGVGGGSVAQVFGNSFGNODPPLDPRVNSALSGSR 729
QY 530 -----GQGFGEAMVLLSDKATSPSLSDAGLQGA 557
Db 730 ALSNHLMSAPRGNFRPAMPRPNLGSDRDCGSEBDELISLSADSGQTEBDF--RY 786
QY 558 PMSDLLMALLLNRAQMAFYFWMGSAVASALGACLLLRVAPLRP---DAEAPARK 613
Db 787 PYSELMIMAVLTFKQDMAQCMQHGEEAMAKALVACRLYKSLATEAEDYLEVEICEELK 846
QY 614 DLAFKREKGVULFGECSSESVBARLLRRCPLMGDATTCLQAMQADARAFPAQDVQ 673
Db 847 KVAEEFRILSLDLHCYHVDACQTLQTLTYELSNNSNEFCALAVIVNNKHLAPCCQ 906
QY 674 SLTQCFWMDMASTT-PIVALYAFPCPLLYTRLTTPKRSBE--EP-TRBELFDMQ- 727
Db 907 ILLADIMHGLMRHTSNIKVILGLCPPI--QMLEFTREBLNLQPGTAAHNDQMAV 964
QY 728 ----SVINGEFGVTADPA-----EKTPLG----- 748
Db 965 SSSSSSSSSSSSSSSSSSSSFEEDDDENNANHDQKTRKTSQSGAQSILNTSLFHSRR 1024
QY 749 -----VPROSGRGCCGG-----RCGGR----- 766
Db 1025 KRAKNEKCDRETDAACAGNRQIQNGGLTBYGTGSGNGVSPPPPYRANRSRRYNN 1084
QY 767 -----RCLRRMFHFWGAPVT 782
Db 1085 RSDMSKTSVIFGSDPNLSKLQKSNITSDRNPMQFGQTRKIKRRRRFYEYSAPISr 1144
QY 783 FNGNVSVYLLFLLESFVLLVDFOPAPGSLR--LLIYFWAFLTCLBELRQGLSGGGSL 840
Db 1145 FMSWTISFLITFTFYTLTPPRPT-VIEYILAVYAAFGI--EQRKTI-----M 1195
QY 841 ASGGPGRGASLSQRLRYLADSNQCDLVALTCLPLGVGCRLTPLGHLGRTVLCIDFM 900
Db 1196 SDKP-----FYEKIRTVCSFMCNCTTILATITFYVGFPMRCF--GSVAYGRVILACDSV 1248
QY 901 VFTRLHLFTVVKQJQPKIVISKMKQDVFPFLPFLGYMLVAVGVATEGLLRPRDSEP 960
Db 1249 LWTMKLDVMSVHPKGFVYVMAKMIQMSYIIVLVLTLSFGIARQSTIYPRDSTWIM 1308
QY 961 SIIRRVFRPYQIQFQIPQEDMDVALMEHNSCSSEPGWAH-----PRGAQAGT 1010
Db 1309 ILVRNIFLPRYMLYGEVYADEID-----TCGDEA--WDQHLENGSPVILGNGTGTGS 1359
QY 1011 CYSQVAMNLVLLVILVIANILLVNLILAMPSTYFGVQNSDLTYMKARVRLIRBP 1070
Db 1360 CVPGY--WIPLLMTFFLIANILMSMLIALFNHFDATDEMSQIQMLPORKQVMEYS 1417
QY 1071 SRPALAPFIVISHLRL-----RQLCRPRSPQSPSPALBHFVYLSKEARLLTWE 1125
Db 1418 STPFLPPLTPLYHGLIILQFTRILSCSKSGERNIL-LIKAIELFLNDQIEKLHDE 1476
QY 1126 SVHKNFLLIARADKRESDESLKRTSQVDLAKQL-----GHIREYORLKY 1174
Db 1477 BOCMEDIAQKNEKNTSNEQRIILRADIRTDQILNRLIDQAKESGARDVINVESRLAS 1536
QY 1175 LRR---EVQCGSRVL---GWVAELSRSLALRP-----GPPPP---DLPGS 1212

CC extracellular calcium influx into their SOC/CRAc-expressing cells. They
 CC will also be useful for delivering therapeutic and/or imaging agents to
 CC such cells to modulate proliferation and growth. SOC/CRAc polypeptides
 CC also represent targets for designing and/or identifying inhibitors that
 CC block lymphocyte proliferation and binding agents that selectively bind
 CC to SOC/CRAc polypeptides to which drugs or toxins can be conjugated for
 CC delivery to SOC/CRAc expressing cells. Methods for determining the level
 CC of SOC/CRAc expression in a subject can be used to assess the presence,
 CC or absence, or stage of a proliferative disorder, e.g. a lymphocyte
 CC proliferative disorder

XX Sequence 1214 AA;

Query Match 100.0%; Score 6383; DB 3; Length 1214;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPPEKQSWI PKI FKKKCTTPIVDSTDPGTLCCGGRPTAHPAVAMEDAFGAAVTV 60
 DB 1 MNPPEKQSWI PKI FKKKCTTPIVDSTDPGTLCCGGRPTAHPAVAMEDAFGAAVTV 60
 QY 61 WDSDAHTTEKPTDAGVGLDPTGAGRKSNFLRSDRDPAAVSVLVRTWGFPAPNLVVS 120
 DB 61 WDSDAHTTEKPTDAGVGLDPTGAGRKSNFLRSDRDPAAVSVLVRTWGFPAPNLVVS 120
 QY 121 VLGGSGPVLQTMLODLRLRGLVRAAOSTGAMIVTGGLHTGIGHVGVAAVRDHOMASTGC 180
 DB 121 VLGGSGPVLQTMLODLRLRGLVRAAOSTGAMIVTGGLHTGIGHVGVAAVRDHOMASTGC 180
 QY 181 TKVAVAMVAMGVVNRNDTLINPKSPARYRMRGDEPDGVOPFLDYNASAPFLVDGTH 240
 DB 181 TKVAVAMVAMGVVNRNDTLINPKSPARYRMRGDEPDGVOPFLDYNASAPFLVDGTH 240
 QY 241 GCLGGERPFLRLSESYTSOQKTGVGCTGIDIPVLLLIIDDEKRLTIENATQALPCLL 300
 DB 241 GCLGGERPFLRLSESYTSOQKTGVGCTGIDIPVLLLIIDDEKRLTIENATQALPCLL 300
 QY 301 VAGSGAADCLAELEDTLAPGSGAGQGEARDRIRFPFKGDELEVQAVERIMTRKEL 360
 DB 301 VAGSGAADCLAELEDTLAPGSGAGQGEARDRIRFPFKGDELEVQAVERIMTRKEL 360
 QY 361 LTVYSSSEKGSBEPETIYLKALVKACSSSEASAYLDELRLAVANNRVDIAOSLFRGDIQW 420
 DB 361 LTVYSSSEKGSBEPETIYLKALVKACSSSEASAYLDELRLAVANNRVDIAOSLFRGDIQW 420
 QY 421 RSFHLKSLMDALLNDRPEFVRLIISGLSLGHFLTQMRLAQLYSAPNSILRNLLDOA 480
 DB 421 RSFHLKSLMDALLNDRPEFVRLIISGLSLGHFLTQMRLAQLYSAPNSILRNLLDOA 480
 QY 481 SHSAGTKAPALKGGAAELRPDVGHVLRMLLKKACARYPSGGAMDHPGQGESMYTL 540
 DB 481 SHSAGTKAPALKGGAAELRPDVGHVLRMLLKKACARYPSGGAMDHPGQGESMYTL 540
 QY 541 SDRKATSPSLIDAGLQAPMSDLLLWALLNRAQAAVYFWEMGSAVSSALGACLLRVMA 600
 DB 541 SDRKATSPSLIDAGLQAPMSDLLLWALLNRAQAAVYFWEMGSAVSSALGACLLRVMA 600
 QY 601 RLEPDAEBAARRDLAKFEGMGVDLFGECYRSSEVAAALLRLRCCLMDATCLOLAMO 660
 DB 601 RLEPDAEBAARRDLAKFEGMGVDLFGECYRSSEVAAALLRLRCCLMDATCLOLAMO 660
 QY 661 ADARAFAPQDVOSLTLQKMGDMASTPIWALVAFPCPLIYTRILTRKSEEBETRE 720
 DB 661 ADARAFAPQDVOSLTLQKMGDMASTPIWALVAFPCPLIYTRILTRKSEEBETRE 720
 QY 721 ELEPDMDSVINGEGPVGTADPAEKTPVGVPRQSGRPGCCGGRCLLRWHPFGAPV 780
 DB 721 ELEPDMDSVINGEGPVGTADPAEKTPVGVPRQSGRPGCCGGRCLLRWHPFGAPV 780
 QY 781 TIFMGVNVSYLLPLLFSSVLLVDFOPAPPGSLLELLIYFAFTLLCEELACQISGGGSL 840
 DB 781 TIFMGVNVSYLLPLLFSSVLLVDFOPAPPGSLLELLIYFAFTLLCEELACQISGGGSL 840

QY 841 ASGSGPGRHSLISQRLRLYLADSWNOCDLVALTCFLGVGCRITPGLYHLGRTVLCIDFM 900
 DB 841 ASGSGPGRHSLISQRLRLYLADSWNOCDLVALTCFLGVGCRITPGLYHLGRTVLCIDFM 900
 QY 901 VFPVRLIHTFTNNKQIGPKIVIVSKMKDVPPFLPFLGVLVAVGATGILRPRSDPP 960
 DB 901 VFPVRLIHTFTNNKQIGPKIVIVSKMKDVPPFLPFLGVLVAVGATGILRPRSDPP 960
 QY 961 SIIRRVFVRPYLQIFQOIPQEDMDVALMEHNSCSSRPGFWAMPGAQAGTSQVYANMLV 1020
 DB 961 SIIRRVFVRPYLQIFQOIPQEDMDVALMEHNSCSSRPGFWAMPGAQAGTSQVYANMLV 1020
 QY 1021 VLLVIFELVAVNLLVNLVLIAMPSTYFGKQVNSDLYMKAQRVRLIRFHSRPAALAPP 1080
 DB 1021 VLLVIFELVAVNLLVNLVLIAMPSTYFGKQVNSDLYMKAQRVRLIRFHSRPAALAPP 1080
 QY 1081 VISHRLRLRLQLCRRRSPSPSSPALSHRVVYSKAEKRLTWESVHKENFLAARDK 1140
 DB 1081 VISHRLRLRLQLCRRRSPSPSSPALSHRVVYSKAEKRLTWESVHKENFLAARDK 1140
 QY 1141 RESDSRLKRTSQKVDLALKQIGHIREYBQRLKVLREYQQGSRVGVVABALRSALLP 1200
 DB 1141 RESDSRLKRTSQKVDLALKQIGHIREYBQRLKVLREYQQGSRVGVVABALRSALLP 1200
 QY 1201 PGSPPPDLPGSKD 1214
 DB 1201 PGSPPPDLPGSKD 1214

RESULT 2
 ADH62712
 ID ADH62712 standard; protein; 1214 AA.

XX ADH62712;

XX 25-MAR-2004 (first entry)

XX Ca activated nonselective transmembrane channel protein TRPM4b.

XX bioactive agent; monovalent cation permeability; TRPM4b channel; human;

XX calcium activated nonselective transmembrane channel.

XX Homo sapiens.

XX US2003143557-A1.

XX 31-JUL-2003.

XX 08-MAY-2002; 2002US-00142649.

XX 25-JAN-2002; 2002US-0351938P.

XX 02-MAY-2002; 2002US-0377937P.

XX (PENN/) PENNER R.

XX Penner R;

XX WPI; 2003-829785/77.

XX N-PSDB; ADH62711.

XX Screening for candidate bioactive agents involves contacting calcium-

XX TRPM4b with candidate agent, determining binding of candidate agent

XX Claim 4; SEQ ID NO 2; 25pp; English.

XX The invention describes a method of screening (M1) for a candidate

XX bioactive agent (CA) modulating monovalent cation (MC) permeability of

XX the TRPM4b (I) channel. The method involves providing a recombinant cell

XX (RC) with a nucleic acid encoding (I) and an inducible promoter operably

XX linked to (I), capable of expressing (I), and comprises an MC indicator,

XX inducing RC to express (I), contacting RC with MC and CA, and detecting

Query Match	75.7%	Score 2758;	DB 11;	Length 3118;
Best Local Similarity	88.5%	Pred. No. 0;		
Matches 2758; Conservative	0;	Mismatches 360;	Indels 0;	Gaps 0;

[illegible]

QY	1603	TAAGAGCAATGTAATCTGCTCTCCGACAAGGCCACCTCGCCGCTCTGCTGGAGATGCTGGCCCTC	1662
Db	1081	GAGACCAATGTAATCTGCTCTCCGACAAGGCCACCTCGCCGCTCTGCTGGAGATGCTGGCCCTC	1140
QY	1663	GAGCAGAGCCCCCTGAGAGCACTGCTCTTTTGGAGCACTGTTGGAGTAACAGAGGCACAGATG	1722
Db	1141	GAGCAGAGCCCCCTGAGAGCACTGCTCTTTTGGAGCACTGTTGGAGTAACAGAGGCACAGATG	1200
QY	1723	GCATATGTACTTCTGAGAGATGAGGTTCACAAATGCAATGCTCTCAGCTCTTGGAGCCTGTTTG	1782
Db	1201	GCATATGTACTTCTGAGAGATGAGGTTCACAAATGCAATGCTCTCAGCTCTTGGAGCCTGTTTG	1266
QY	1783	CTGCTCCGGGAGATGAGCACCGCTGTGAGGCTGTACCGCTAGAGAGGAGACACGAGAAAGAC	1842
Db	1261	CTGCTCCGGGAGATGAGCACCGCTGTGAGGCTGTACCGCTAGAGAGGAGACACGAGAAAGAC	1320
QY	1843	CTGAGGCTTCAAGTTTAGAGGGAGTGGAGGCTTGACCTCTTGGCGAGGTGTAATCGACAGCT	1902
Db	1321	CTGAGGCTTCAAGTTTAGAGGGAGTGGAGGCTTGACCTCTTGGCGAGGTGTAATCGACAGCT	1380
QY	1903	GAGGTGAGGGCTGCCCCGCTCTCTCCCTCGATCGATGCCGCTCTGAGGGAGATGCCACTTGC	1962
Db	1381	GAGGTGAGGGCTGCCCCGCTCTCTCCCTCGATCGATGCCGCTCTGAGGGAGATGCCACTTGC	1440
QY	1963	CTCCAGCTGACATGCAAGCTGACGCGCCGTGCTCTTCTTGCCAGATGAGGGTACAGTCT	2022
Db	1441	CTCCAGCTGACATGCAAGCTGACGCGCCGTGCTCTTCTTGCCAGATGAGGGTACAGTCT	1500
QY	2023	CTGCTGACACAGAAATGAGTGGTGGGGAGATATGAGCGACACTACACCACATCTGGAGCCCTGGTT	2082
Db	1501	CTGCTGACACAGAAATGAGTGGGGAGATATGAGCGACACTACACCACATCTGGAGCCCTGGTT	1560
QY	2083	CTGCGCTTCTTTTGCCCTCCACTCATCTATACACCCGCTCATACCTTCAGAGAAATCAGAA	2142
Db	1561	CTGCGCTTCTTTTGCCCTCCACTCATCTATACACCCGCTCATACCTTCAGAGAAATCAGAA	1620
QY	2143	GAGAGGCCACACAGAGAGAGACTGATGTTGACATGATATGCTCATTTATGGGAAAGG	2202
Db	1621	GAGAGGCCACACAGAGAGAGACTGATGTTGACATGATATGCTCATTTATGGGAAAGG	1680
QY	2203	CCTGTCCGAGAGAGGGAGAGCCACAGCCGAGAAAGCGCGCTGAGGGAGTCCGCGCBACTCGAGG	2262
Db	1681	CCTGTCCGAGAGAGGGAGAGCCACAGCCGAGAAAGCGCGCTGAGGGAGTCCGCGCBACTCGAGG	1740
QY	2263	CGTCCGAGGTTTCTGTCGAGGAGCGCGCTGCGAGGAGGCGCGAGTGCCTACACCGCTGTTCCAC	2322
Db	1741	CGTCCGAGGTTTCTGTCGAGGAGCGCGCTGCGAGGAGGCGCGAGTGCCTACACCGCTGTTCCAC	1800
QY	2323	TTCTGAGGAGCGGCGCGGTGACCATCTTCAATGAGCAAGTGTGACGTACCTGCTGTTCTG	2382
Db	1801	TTCTGAGGAGCGGCGCGGTGACCATCTTCAATGAGCAAGTGTGACGTACCTGCTGTTCTG	1860
QY	2383	CTGCTTTTCTGCGAGGAGTGTGCTGTGTGGAATTTCCAGCCGAGCGCGCCGCTCCCTGAG	2442
Db	1861	CTGCTTTTCTGCGAGGAGTGTGCTGTGTGGAATTTCCAGCCGAGCGCGCCGCTCCCTGAG	1920
QY	2443	CTGCTGCTCTATTTCTGAGGCTTTTCAACGCTGTGTGCGAGGAACTGCGCAGAGGCTGAGC	2502
Db	1921	CTGCTGCTCTATTTCTGAGGCTTTTCAACGCTGTGTGCGAGGAACTGCGCAGAGGCTGAGC	1980
QY	2503	GAGAGCGAGGAGCAGCTTCGCCAGCGAGGAGGCTCCGAGCTTGCCATATGCTTACCTAGGCAG	2562
Db	1981	GAGAGCGAGGAGCAGCTTCGCCAGCGAGGAGGCTCCGAGCTTGCCATATGCTTACCTAGGCAG	2040
QY	2563	CGCTCGGCTCTTACCTTCGCCAGCAGCTTGGAACCATGTGCCACTTATGTGCTCTACCTGC	2622
Db	2041	CGCTCGGCTCTCTACCTTCGCCAGCAGCTTGGAACCATGTGTGCTCTACCTGC	2100
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Dd	1030	GAACAGCGCTGAAAGTGTGAGAGCGGAGGTCCAGCAGTGTAGCCGCGTCTTGAGGTGG	1089
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Db      1150 CTGCCTGGGTCCTCAAGAC 1167
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RESULT 2
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEO ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-109

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Best Local Similarity 100.0%; Pred. No. 2,66-249; Indels 0; Gaps 0;
Matches 1158; Conservative 0; Mismatches 0;

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2665 CACCTGGGCGCAGCTGTCTCTGATGATGACTTTCATGTTTTCACGAGCGGCTGCTTAC 2724
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OW nucleic - nucleic search, using sw model

Run on: January 6, 2006, 09:03:31 ; Search time 1922 Seconds

(without alignment)
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	3642	100.0	4061	ADSL2774
6	3642	100.0	4061	ADSV9224
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8	3498	96.0	3501	ABK92224
9	3498	96.0	3501	ADN9597
10	3498	96.0	4641	ADN95239
11	3473.8	95.4	3898	ADL06463
12	3421.2	93.9	3810	ABK92167
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15	3421.2	93.9	3810	ADR66772
16	3374.4	92.7	3900	AAH76383
17	3374.4	92.7	3900	ABBS58041
18	3374.4	92.7	3900	ADH51622
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22	3199.8	87.9	3676	12	ADQ83682	Adq83682 Human tum
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25	3196.6	87.8	3701	13	ADSL2776	Adsl2776 Transient
26	3052	83.8	3583	11	ADL33391	Adl33391 Human tra
27	2269.4	62.3	2695	6	AAAD3373	AAad3373 Human Trp
28	2073.4	56.9	2459	12	ADL06424	Adl06424 Human tum
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ALIGNMENTS

RESULT 1	ACL38958	standard; CDNA; 4001 BP.
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AC	ACL38958	
DT	24-MAR-2005	(first entry)
XX	TRPM4 coding sequence, SEQ ID 15.	
DB	TRPM4 coding sequence, SEQ ID 15.	
XX	Cytosolic; Gene therapy; Vaccine; RNA interference; cancer; gene; ss.	
XX	Homo sapiens.	
OS	WO200501092-A2.	
XX	06-JAN-2005.	
PD	19-MAY-2004; 2004WO-US015645.	
XX	19-MAY-2004; 2003US-0471729P.	
PF	20-MAY-2003; 2003US-0471729P.	
XX	(AMHP) WYETH.	
PA	Be X, Wei L, Slonim DK, Howes SH;	
PI	WPI; 2005-075568/08.	
XX	P-PSDB; ABR99976.	
DR	Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABC4, or a T cell	
XX	activated by the polypeptide or antibody, and a carrier, useful for	
PT	treating cancer.	
PT	claim 8; SEQ ID NO 15; 113pp; English.	
XX	The present invention relates to a novel pharmaceutical composition	
XX	comprising: (a) an agent capable of modulating an expression level or	
CC	protein activity of a cancer-related transmembrane protein (CRTP) or gene	
CC	; an antibody specific for a CRTP, or a T cell activated by a CRTP; and	
CC	(b) a carrier. The pharmaceutical composition may also comprise a	
CC	polynucleotide capable of inhibiting or decreasing the expression of the	

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 09:10:27 ; Search time 17521 Seconds
(without alignments)
11815.755 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Displaying first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	3421.2	93.9	3810	6	CO896241 Sequence
7	3421.2	93.9	3810	8	AK000048 Homo sapi
8	3374.4	92.6	3900	6	AX235183 Sequence
9	3373.8	92.6	3387	6	AX235185 Sequence
10	3333	91.5	3402	6	CQ715325 Sequence
11	3253.4	89.3	3599	6	AX402516 Sequence
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13	3196.6	87.8	3701	8	AY046396 Homo sapi
14	2762	75.8	3444	8	AY297046 Homo sapi
15	2424	66.6	3800	9	MM0575814 Mus muscu
16	2419.2	66.4	4053	9	BC096475 Mus muscu
17	2269.4	62.3	2695	6	AX443225 Sequence
18	2196.8	60.3	2981	8	AK000235 Homo sapi

19	2089.2	57.4	3725	9	BC049165 Mus muscu
20	1935.6	53.1	2157	8	AB097553 Macaca fa
21	1911	52.5	2393	6	BD082082 Reagents
22	1892.2	52.0	2180	6	BD270154 Character
23	1660.2	45.6	2993	9	BC058632 Mus muscu
24	1471.6	40.4	2737	9	BC046472 Mus muscu
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37	1158	31.8	1524	6	AR563607 Sequence
38	1158	31.8	1524	6	AR588593 Sequence
39	1158	31.8	1524	6	AR605413 Sequence
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ALIGNMENTS

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ACCESSION	AY297045	GI:31335332			
VERSION	AY297045.1	GI:31335332			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 3879)				
AUTHORS	Hofmann, T., Chubrov, V., Gudermann, T. and Montell, C.				
TITLE	TRPM5 is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel				
JOURNAL	Curr. Biol. 13 (13), 1153-1158 (2003)				
PUBMED	12842017				
REFERENCE	2 (bases 1 to 3879)				
AUTHORS	Chubrov, V., Hofmann, T., Gudermann, T. and Montell, C.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAY-2003) Institut fuer Pharmakologie und Toxikologie, Phillips-Universitaet Marburg, Karl-von-Friesch-Strasse 1, Marburg D-35033, Germany				
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ORIGIN

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QY 901 GTGGCTGGCTCAGGGGGAGACTGGGACTGCGGACTGCGCGGAGACCTTGGAAAGACATGGGCG 960
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DB 1013 CCAAGGAGTGGGGAGACCAAGGCAAGGCGGAAGCCGAGATCGAATCAGGCGCTTCTTCC 1072
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QY 1141 CTGTGAAGGCTGTGGAGACTCGAGAGCTCAGCTTACCTGATGATGCTGCTTGGCT 1200
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QY 1201 GTGGCTTGAAGCCGCTGAGACATTTGCCAGAGTGAATCTTTTGGGGGAGACATCCAAATGG 1260
DB 1253 GTGGCTTGAAGCCGCTGAGACATTTGCCAGAGTGAATCTTTTGGGGGAGACATCCAAATGG 1312
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QY 1321 GTGCGCTTCTCATTTCCACGCGCTCAGCTTGGGCACTTCTGACCCCGATGCGCTG 1380
DB 1373 GTGCGCTTCTCATTTCCACGCGCTCAGCTTGGGCACTTCTGACCCCGATGCGCTG 1432
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QY 1681 GACCTGCTTCTTGGGACATGTTGCTGAACAGGGGCAAGATGGCCATGATCTTCTGGAG 1740
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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 6, 2006, 08:59:09 ; Search time 651 Seconds
(without alignments)
11088.599 Million cell updates/sec

Title: US-09-869-486B-29

Perfect score: 4061
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1505	37.1	1524	US-09-030-607-109	Sequence 109, App
3	1505	37.1	1524	US-09-439-313-109	Sequence 109, App
4	1505	37.1	1524	US-09-352-616A-109	Sequence 109, App
5	1505	37.1	1524	US-09-232-149A-109	Sequence 109, App
6	1505	37.1	1524	US-09-159-812-109	Sequence 109, App
7	1505	37.1	1524	US-09-636-215-109	Sequence 109, App
8	1505	37.1	1524	US-09-685-166A-109	Sequence 109, App
9	1505	37.1	1524	US-09-115-453-109	Sequence 109, App
10	1505	37.1	1524	US-09-688-489-109	Sequence 109, App
11	1505	37.1	1524	US-09-759-143-109	Sequence 109, App
12	1505	37.1	1524	US-09-651-236-109	Sequence 109, App
13	1505	37.1	1524	US-09-030-606-109	Sequence 109, App
14	1505	37.1	1524	US-09-657-279-109	Sequence 109, App
15	1505	37.1	1524	US-10-012-896-109	Sequence 109, App
16	1505	37.1	1524	US-08-727-688-9	Sequence 109, App
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37	429.6	10.6	6220	3	US-09-949-016-470	Sequence 5229, App
38	428	10.5	6221	3	US-09-949-016-5229	Sequence 5229, App
39	395.8	9.7	801	3	US-09-020-956-9	Sequence 9, Appli
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44	395.8	9.7	801	3	US-09-636-215-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-020-956-109
Sequence 109, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-109

Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY	2677	CTAAGTGGCTTCACTTGGTCTCTCTTGGGCGTGGGCTGCGGCTGACCCCGGGTTTGTAC	2736
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OY	2797	ATCTTCACGGTCAACAAACAGCTGGGGGCCAAGATCGTATCGTGGACAAATGATGAAG	2856
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Db	310	GACGTGTTCTTCTTCTTCTTCTTCTTCTTCTGCGCGTGTGGCTGGTAAAGCTTATGCGTGGCACG	369
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Db	430	CGTCCCTACCTGCAATCTTCCGGGAGATTTCCCGAGAGGACATGGAAGTGGGCGCTCATG	489
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QY      3757 ATTTTGTCCCTAAGAGTAAAGGCTCATCTGGGCTCGGCCCCCGGCACTGTGGCTTGTCC 3816
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QY      3937 CCTGATCTCCGGGCGCTTATCATCTGAGGCTGCAAGGCTCTTGGGGTAAACAGGACCA 3996
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; Sequence 109, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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[illegible]

XX The present sequence is a full-length nucleotide sequence of human SOC-3/CRA-2 cDNA. It includes an open reading frame encoding SOC-3/CRA-2 (see AAY9436), a member of a novel family of store operated channel (SOC) or calcium release activated channel (CRAC) polypeptides that modulate Ca^{2+} flux into and out of a cell, and which may be activated upon depletion of Ca^{2+} from intracellular calcium stores, allowing Ca^{2+} influx into a cell. SOC-3/CRA-2 is expressed predominantly in kidney and colon. Compositions for expressing SOC/CRA-2 calcium channel polypeptides in cells may be useful for treating patients that have reduced extracellular calcium influx into their SOC/CRA-2-expressing cells. They will also be useful for delivering therapeutic and/or imaging agents to such cells to modulate proliferation and growth. SOC/CRA-2 polypeptides also represent targets for designing and/or identifying inhibitors that block lymphocyte proliferation and binding agents that selectively bind to SOC/CRA-2 polypeptides to which drugs or toxins can be conjugated for delivery to SOC/CRA-2-expressing cells. SOC/CRA-2 polynucleotides are used as probes and primers to identify other members of the SOC/CRA-2 family of calcium channels, as diagnostic reagents for identifying the presence of SOC/CRA-2 polypeptides in biological samples, as agents for generating SOC/CRA-2 binding polypeptides, and in gene therapy. Methods for determining the level of SOC/CRA-2 expression in a subject can be used to assess the presence, or absence, or stage of a proliferative disorder, e.g. a lymphocyte proliferative disorder.

XX Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 4061; DB 3; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 TGTGGGCGCCCGGAGCCGCCAAGTGGCATGAGAGATGCTTTGCGGCGAGCC 240
QY 241 GTGGTGAACGATGAGGAGACAGGATGACACACAGGAGAGCCAGATGCGTACGGA 300
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QY 481 CTGCT 540
Db 481 CTGCT 540
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Db 1621 CCGAGGTAACCTTCGAGGAGGAGCTGAGGACCTTACCAAGGAGGAGGCTTCCGAGAGAGC 1680
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GenCore version 5.1.6
(c) 1993 - 2006 Compu

; Search time 19870 Seconds

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residues

ameters: 11766282

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IES

Description
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AF497623 Homo sapi
AJ575813 Homo sapi
AX443227 Sequence
AY297045 Homo sapi
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ALIGNMENTS

ear PAT 17-JUL-2003
ata, Euteleostomi;
Cabarrhini;
25, A6IK35/76, A6IK38/
A6IP3/14, A6IP43/00,
5/10, C12Q1/48, C12Q1/
C12N15/00, C12N5/00,
ILY
' . (human)' .

ORIGIN

Query Match 100.0%; Score 4061; DB 6; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION Pan troglodytes TRPM4 gene, VIRIDAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DO031082
VERSION DO031082.1 GI:6688286
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE 1 (bases 1 to 2532)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeille,D.,

GenCore version 5.1.6
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Run on: January 6, 2006, 08:58:54 ; Search time 410 Seconds
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Minimum DB seq length: 0
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Listing: First 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1149.8	52.7	1524	3	US-09-030-607-109 Sequence 109, App
3	1149.8	52.7	1524	3	US-09-439-313-109 Sequence 109, App
4	1149.8	52.7	1524	3	US-09-352-616A-109 Sequence 109, App
5	1149.8	52.7	1524	3	US-09-232-149A-109 Sequence 109, App
6	1149.8	52.7	1524	3	US-09-159-812-109 Sequence 109, App
7	1149.8	52.7	1524	3	US-09-636-215-109 Sequence 109, App
8	1149.8	52.7	1524	3	US-09-685-166A-109 Sequence 109, App
9	1149.8	52.7	1524	3	US-09-115-453-109 Sequence 109, App
10	1149.8	52.7	1524	3	US-09-688-489-109 Sequence 109, App
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12	1149.8	52.7	1524	3	US-09-759-143-109 Sequence 109, App
13	1149.8	52.7	1524	3	US-09-651-236-109 Sequence 109, App
14	1149.8	52.7	1524	3	US-09-030-606-109 Sequence 109, App
15	1149.8	52.7	1524	3	US-09-657-279-109 Sequence 109, App
16	1149.8	52.7	1524	3	US-10-012-896-109 Sequence 109, App
17	1149.8	52.7	1524	3	US-08-727-688-9 Sequence 109, App
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ALIGNMENTS

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; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillian, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-109
Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 6e-245;
Matches 125; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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DB 550 GGCACCTGCGTCTCCAGATAGCCCACTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 609
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DB 610 CTGCGGCGCAATCTGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 669
QY 1513 AAAGTACAGGGGCAAGCGATCTCTAAGAGGCGGAGCGGTTACCGGCTCATCGGGAA 1572
DB 670 AAAGTACAGGGGCAAGCGATCTCTAAGAGGCGGAGCGGTTACCGGCTCATCGGGAA 729
QY 1573 TTCACTCTGCGCGCGGCTGAGCGGCGGCGGCTTATGCTGATCTGCTGCTGCTGCTGCTG 1632
DB 730 TTCACTCTGCGCGCGGCTGAGCGGCGGCGGCTTATGCTGATCTGCTGCTGCTGCTGCTG 789
QY 1633 CTGAGGCAATTTGAGGAGGAGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1692
DB 790 CTGAGGCAATTTGAGGAGGAGCGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 849
QY 1693 TTCCGGGTTTACCTTTCTAAGAGAGCGGAGCGGAGCTGCTAAGCTGGGAACTGGTGCAT 1752
DB 850 TTCCGGGTTTACCTTTCTAAGAGAGCGGAGCGGAGCTGCTAAGCTGGGAACTGGTGCAT 909
QY 1753 AAGAGAACTTTGCTGCTGAGCGGCTTGGAGCAAGCGGAGAGAGGACTCCGAGGCTGCTG 1812
DB 910 AAGAGAACTTTGCTGCTGAGCGGCTTGGAGCAAGCGGAGAGAGGACTCCGAGGCTGCTG 969
QY 1813 AAGGCACTGCTCCAGAGGAGGAGCTTGGAGCAAGAGCTGGGAGCACTCCGAGGCTGCTG 1872
DB 970 AAGGCACTGCTCCAGAGGAGGAGCTTGGAGCAAGAGCTGGGAGCACTCCGAGGCTGCTG 1029
QY 1873 GAACAGCGCTGAAAGTCTGAGGCGGAGGCTCCAGAGTGA----- 1915
DB 1030 GAACAGCGCTGAAAGTCTGAGGCGGAGGCTCCAGAGTGAAGCGGCTGCTGAGGCTGCTG 1089
QY 1916 ----- 1915

DB 1090 GTGGCGAGGCGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
QY 1916 ----- 1915
DB 1150 CTGCGTGGGTCAAGAGCTGAGCGGCTGCTGCGGAGCTTCAAGAGAGAGAGAGAGAGAGAG 1209
QY 1916 -----CTGCGGCGCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1945
DB 1210 ATTTGCTCTAGAGTGAAGCTGATGAGGCTGAGGCTGAGGCGCGCGGAGCTGAGGCTTGGCT 1269
QY 1946 TTGAGTGAAGGCGGAGTGCATGAGGCGGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGG 2005
DB 1270 TTGAGTGAAGGCGGAGTGCATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1329
QY 2006 TTACAAACACAGAGATCCCGGCTCTCCAGAGACAGTCCAGGCTGGAGGAGTCAAGG 2065
DB 1330 TTACAAACACAGAGATCCCGGCTCTCCAGAGACAGTCCAGGCTGGAGGAGTCAAGG 1389
QY 2066 CTGAGATCCCGGCGGTTATTCATCTGAGAGGCTGAGGAGGCTTGGGAGTCAAGGAGCA 2125
DB 1390 CTGAGATCCCGGCGGCTTATTCATCTGAGAGGCTGAGGAGGCTTGGGAGTCAAGGAGCA 1449
QY 2126 CAGAGCGGCTGAGCACTGAGATTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2180
DB 1450 CAGAGCGGCTGAGCACTGAGATTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1504

RESULT 2
US-09-030-607-109
Sequence 109, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-109
Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 6e-245;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2006, 08:58:52 ; Search time 1330 Seconds
(without alignments)
10924.083 Million cell updates/sec

Title: US-09-869-486B-25
Perfect score: 2180
Sequence: 1 tcgagcgccagatcgcgca.....ggagataagccattcaga 2180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Library filter 45 summaries

Database : N(Geneseq 2.1)*
1: geneseqn1980b:*
2: geneseqn1990b:*
3: geneseqn2000b:*
4: geneseqn2001b:*
5: geneseqn2001b:*
6: geneseqn2002b:*
7: geneseqn2002b:*
8: geneseqn2003b:*
9: geneseqn2003b:*
10: geneseqn2003b:*
11: geneseqn2003b:*
12: geneseqn2004b:*
13: geneseqn2004b:*
14: geneseqn2005b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2178.8	99.9	2180	3	AAA49921 Human cal
2	1978.8	99.8	3583	11	ADL33391 Human tra
3	1978.8	90.8	3676	12	ADQ83682 Human tum
4	1978.8	90.8	3676	13	ADQ83682 Human tum
5	1978.8	90.8	3676	13	ADQ83682 Human tum
6	1978.8	90.8	3900	5	AAH76383 Human tra
7	1978.8	90.8	3900	8	ABSS58041 Human tra
8	1978.8	90.8	3900	12	ADH51622 Human 186
9	1978.8	90.8	4001	14	ACL38958 TRPM4 cod
10	1978.8	90.8	4061	3	AAA49923 Human cal
11	1978.8	90.8	4061	10	ADH62711 Ca activa
12	1978.8	90.8	4061	13	ADR73511 Human TRP
13	1978.8	90.8	4061	13	ADSL2774 Transient
14	1978.8	90.8	4061	14	ADV97224 Human cat
15	1978.8	90.8	4641	11	ADN39239 Cancer/an
16	1977.2	90.7	2695	6	AAJ32373 Human Trp
17	1977.2	90.7	4042	6	AAJ32372 Human Trp
18	1975.6	90.6	3810	6	ABK92167 Prostate
19	1975.6	90.6	3810	13	ADR66772 Human pro

20	1975.6	90.6	3810	13	ADR65869	Adt65869 Human pro
21	1975.6	90.6	3810	13	ADSL2778	Adt12778 Human TRP
22	1975.6	90.6	3898	12	ADL06463	Adt06463 Human tum
23	1974	90.6	3701	13	ADSL2776	Adt12776 Transient
24	1968.2	90.3	3599	6	ABK28677	ABK28677 Human CDN
25	1943.8	89.2	2459	12	ADL06424	Adt06424 Human tum
26	1892.2	86.8	3387	5	AAH76384	AAH76384 Human TRC
27	1892.2	86.8	3390	12	ADH51624	Adh51624 Human 186
28	1892.2	86.8	3501	6	ABK92224	ABK92224 Prostate
29	1892.2	86.8	3501	11	ADN39597	Adn39597 Cancer/an
30	1891	86.7	2393	2	AAV26656	AAV26656 Human PSL
31	1891	86.7	2393	3	AAH64090	AAH64090 Consensus
32	1202	55.1	2176	12	ADQ96621	Adq96621 Human PSL
33	1149.8	52.7	1524	2	AAV58585	AAV58585 Prostate
34	1149.8	52.7	1524	2	AAV61200	AAV61200 Full leng
35	1149.8	52.7	1524	3	AAH06348	AAH06348 Human imm
36	1149.8	52.7	1524	3	ABH71253	ABH71253 Human pro
37	1149.8	52.7	1524	4	AAH93464	AAH93464 Human pro
38	1149.8	52.7	1524	4	AAH63556	AAH63556 Human pro
39	1149.8	52.7	1524	4	AAH02529	AAH02529 Prostate
40	1149.8	52.7	1524	4	AAH84778	AAH84778 Human pro
41	1149.8	52.7	1524	5	ACA59365	ACA59365 Prostate
42	1149.8	52.7	1524	5	AAH10107	AAH10107 Human pro
43	1149.8	52.7	1524	6	ABL94928	ABL94928 Human J1-
44	1149.8	52.7	1524	6	ABH58637	ABH58637 Prostate
45	1149.8	52.7	1524	8	ACC95092	ACC95092 Prostate

ALIGNMENTS

RESULT 1	AAA49921	standard; cDNA; 2180 BP.
ID	AAA49921	
XX	AAA49921;	
AC	10-OCT-2000	(first entry)
XX		
DT		
XX		
DE	Human calcium channel SOC-3/CRAC-2 partial cDNA.	
XX		
XX	SOC-3/CRAC-2; calcium channel; human; store operated channel;	
KW	calcium release activated channel; therapy; diagnosis;	
KW	lymphocyte proliferative disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..2180
FT		/*tag= a
FT		/partial
XX		
XX	WO200040614-A2.	
PN		
XX		
PD	13-JUL-2000.	
XX		
PF	20-DEC-1999;	99WO-US029996.
XX		
PR	30-DEC-1998;	98US-0114220P.
PR	29-JAN-1999;	99US-0120018P.
PR	22-JUN-1999;	99US-0140415P.
XX		
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
XX		
PI	Scharenberg AM;	
XX		
DR	WPI; 2000-465957/40.	
XX	P-PSDB; AA95434.	
XX		
PT	New SOC/CRAC calcium channel polynucleotides and polypeptides used to	
PT	diagnose and treat proliferative disorders associated with the channel,	
PT	and to screen for novel modulators of the channel.	

PS Claim 1(a); Page 90-91; 108bp; English.

XX The present sequence is a partial nucleotide sequence of human SOC-3/CRAC
CC -2 cDNA. A partial open reading frame encodes the C-terminal portion (see
CC AY95134) of SOC-3/CRAC-2, a member of a novel family of store operated
CC channel (SOC) or calcium release activated channel (CRAC) polypeptides
CC that modulate Ca²⁺ flux into and out of a cell, and which may be
CC activated upon depletion of Ca²⁺ from intracellular calcium stores,
CC allowing Ca²⁺ influx into a cell. SOC-3/CRAC-2 (full-length cDNA given in
CC AA49923) is expressed predominantly in the kidney and colon.

CC Compositions for expressing SOC/CRAC calcium channel polypeptides in
CC cells may be useful for treating patients that have reduced extracellular
CC calcium influx into their SOC/CRAC-expressing cells. They will also be
CC useful for delivering therapeutic and/or imaging agents to such cells to
CC modulate proliferation and growth. SOC/CRAC polypeptides also represent
CC targets for designing and/or identifying inhibitors that block lymphocyte
CC proliferation and binding agents that selectively bind to SOC/CRAC
CC polypeptides to which drugs or toxins can be conjugated for delivery to
CC SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used as probes
CC and primers to identify other members of the SOC/CRAC family of calcium
CC channels, as diagnostic reagents for identifying the presence of SOC/CRAC
CC polypeptides in biological samples, as agents for generating SOC/CRAC
CC binding polypeptides, and in gene therapy. Methods for determining the
CC level of SOC/CRAC expression in a subject can be used to assess the
CC presence, or absence, or stage of a proliferative disorder, e.g. a
CC lymphocyte proliferative disorder

XX Sequence 2180 BP; 365 A; 694 C; 667 G; 451 T; 0 U; 3 Other;

Query Match 99.9%; Score 2178.8; DB 3; Length 2180;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGGCCAAGATTCGSCACGAGGGCTCGGGCAGGCCCTCGGAGGACCTGTTCTT 60
DB 1 TCGAGGCCAAGATTCGSCACGAGGGCTCGGGCAGGCCCTCGGAGGACCTGTTCTT 60
QY 61 TGGGCATCTGTTGCTGAACAGGACACAGATGGCCATGATCTTGGAGATGGGTTCCAT 120
DB 61 TGGGCATCTGTTGCTGAACAGGACACAGATGGCCATGATCTTGGAGATGGGTTCCAT 120
QY 121 TGGGCATCTGTTGCTGAACAGGACACAGATGGCCATGATCTTGGAGATGGGTTCCAT 180
DB 121 TGGGCATCTGTTGCTGAACAGGACACAGATGGCCATGATCTTGGAGATGGGTTCCAT 180
QY 121 GCACTTTCTCAGCTCTTGGGAGCTGTTGCTGCTCCGGGTGATGCGACGCTTGAGCCT 180
DB 121 GCACTTTCTCAGCTCTTGGGAGCTGTTGCTGCTCCGGGTGATGCGACGCTTGAGCCT 180
QY 181 GACCTGTGAGAGGACGACGAGGAAAGACCTGGCGTTCAAGTTTGAAGGGATGGCGCTT 240
DB 181 GACCTGTGAGAGGACGACGAGGAAAGACCTGGCGTTCAAGTTTGAAGGGATGGCGCTT 240
QY 241 GACCTTTTGGCGAGTGTATGCGACAGTGAAGGTGAGGGCTGCCGCTCTCTCTCCGT 300
DB 241 GACCTTTTGGCGAGTGTATGCGACAGTGAAGGTGAGGGCTGCCGCTCTCTCTCCGT 300
QY 301 CGCTGCCCGCTCTGGGGGGATGSCACTTGGCTCCAGCTGGCGCAGTGAAGCTGAGCCCGT 360
DB 301 CGCTGCCCGCTCTGGGGGGATGSCACTTGGCTCCAGCTGGCGCAGTGAAGCTGAGCCCGT 360
QY 361 GCTCTTTTGGCCAGATGGGGTACAGTCTCTGCTGACACAGAACTGGTGGGAGATATG 420
DB 361 GCTCTTTTGGCCAGATGGGGTACAGTCTCTGCTGACACAGAACTGGTGGGAGATATG 420
QY 421 GCCAGCACTAACCCATCTGGGCTCTGGTTCTCGCTTTCTTTTGGCTTCACTCATCTAC 480
DB 421 GCCAGCACTAACCCATCTGGGCTCTGGTTCTCGCTTTCTTTTGGCTTCACTCATCTAC 480
QY 481 ACCGGCTCATCACTTTCAGGAAATCAGAAAGAGGCCCAACAGGAGAGACTAGATT 540
DB 481 ACCGGCTCATCACTTTCAGGAAATCAGAAAGAGGCCCAACAGGAGAGACTAGATT 540
QY 541 GACATGATATGTATTAATATGAGGAGAGGCTGTGAGGAGAGCCGAGCGAGAG 600
DB 541 GACATGATATGTATTAATATGAGGAGAGGCTGTGAGGAGAGCCGAGCGAGAG 600

QY 601 ACGCGCTGAGGATTCGCCGCGCACTGCGGCGCTCGGGGTGCTGCGGGGCGGCTGCGG 660
DB 601 ACGCGCTGAGGATTCGCCGCGCACTGCGGCGCTCGGGGTGCTGCGGGGCGGCTGCGG 660
QY 661 GGGGGCGGGTCCCAAGCCCGTGTTCATCTTGGGGGCGGCGGGTGAACATCTTATG 720
DB 661 GGGGGCGGGTCCCAAGCCCGTGTTCATCTTGGGGGCGGCGGGTGAACATCTTATG 720
QY 721 GGCACATGATCAGCTACTGCTGTTCTGCTGCTTTTTCGCGGGTCTGCTGAGAT 780
DB 721 GGCACATGATCAGCTACTGCTGTTCTGCTGCTTTTTCGCGGGTCTGCTGAGAT 780
QY 781 TTTCAGCCGGCGCCCGGCTCCCTGAGAGTCTGCTCTATTTCTGGGCTTTTACCGCTG 840
DB 781 TTTCAGCCGGCGCCCGGCTCCCTGAGAGTCTGCTCTATTTCTGGGCTTTTACCGCTG 840
QY 841 CTGTCGAGGAACCTGGGCGAGGGCTGAGGGAGGGGGGAGGCTGCGAGGGGGG 900
DB 841 CTGTCGAGGAACCTGGGCGAGGGCTGAGGGAGGGGGGAGGCTGCGAGGGGGG 900
QY 901 CCCGGGCTGGCCATGCTGCTGAGCCAGCGCTGGCGCTCTACTTCGCCAGAGCTGG 960
DB 901 CCCGGGCTGGCCATGCTGCTGAGCCAGCGCTGGCGCTCTACTTCGCCAGAGCTGG 960
QY 961 AACCATGCGACTGATGCTCTCACTGCTTCTCTGGGCGTGGGCTGCGGCTGAC 1020
DB 961 AACCATGCGACTGATGCTCTCACTGCTTCTCTGGGCGTGGGCTGCGGCTGAC 1020
QY 1021 CCGGGTTTGTACCACTGGGCGGACCTGCTCTGACATTCAGTTTATTCAGGTTG 1080
DB 1021 CCGGGTTTGTACCACTGGGCGGACCTGCTCTGACATTCAGTTTATTCAGGTTG 1080
QY 1081 CGGCTGTTTACATCTTCAAGGCTCAACAAACAGCTGGAGGCCAAGATGTCATGTAAGC 1140
DB 1081 CGGCTGTTTACATCTTCAAGGCTCAACAAACAGCTGGAGGCCAAGATGTCATGTAAGC 1140
QY 1141 AAGATGATGAAGACGTGTTCTTCTCTCTTCTCTGCTGGCGTGTGCTGTAGCTAT 1200
DB 1141 AAGATGATGAAGACGTGTTCTTCTCTCTTCTCTCTGCTGGCGTGTGCTGTAGCTAT 1200
QY 1201 GGGCTGGCCACGAGGGGGCTCTGAGGSCAGGGGACAGTGAAGCTTCCAAAGTATCTTGCGC 1260
DB 1201 GGGCTGGCCACGAGGGGGCTCTGAGGSCAGGGGACAGTGAAGCTTCCAAAGTATCTTGCGC 1260
QY 1261 CGGCTTTTCTAACCGTCTCCTACCTGACAGATCTTGGGAGATTTCCAGAGAGATGAGC 1320
DB 1261 CGGCTTTTCTAACCGTCTCCTACCTGACAGATCTTGGGAGATTTCCAGAGAGATGAGC 1320
QY 1321 GTGGCCTCATGAGGACACAGCAATGCTGTCGAGAGCCCGGCTTGTGGGACACCTCTCT 1380
DB 1321 GTGGCCTCATGAGGACACAGCAATGCTGTCGAGAGCCCGGCTTGTGGGACACCTCTCT 1380
QY 1381 GGGGCCAGAGGGGACACTGCGGTCTCCAGATGSCAACTGGCTGTGATGCTGCTCTC 1440
DB 1381 GGGGCCAGAGGGGACACTGCGGTCTCCAGATGSCAACTGGCTGTGATGCTGCTCTC 1440
QY 1441 GTCATCTTCTGCTGTCGTCGCAACATCTGTCCTCACTTGTCTCATTTGCCATGTTAGT 1500
DB 1441 GTCATCTTCTGCTGTCGTCGTCGCAACATCTGTCCTGTCATTTGTCTCATTTGCCAT 1500
QY 1501 TACACATTCGGCAAGTACAGGGGACAGAGATCTTACTGAGGAGGGGACAGCTTACCGC 1560
DB 1501 TACACATTCGGCAAGTACAGGGGACAGAGATCTTACTGAGGAGGGGACAGCTTACCGC 1560
QY 1561 CTCACTCGGGGAATTCACCTCGGCGCGGCTGGCGCCGCTTATATGATATCTCCAC 1620
DB 1561 CTCACTCGGGGAATTCACCTCGGCGCGGCTGGCGCCGCTTATATGATATCTCCAC 1620
QY 1621 TTGGCCTCTCTGCTCAGGCAATTTGTGAGGAGGACCCGAGCGCTCTCTCCCG 1680
DB 1621 TTGGCCTCTCTGCTCAGGCAATTTGTGAGGAGGACCCGAGCGCTCTCTCCCG 1680
QY 1681 GCCTCGAGCAATTTCCGGGTTTACCTTTCTTAAGGAGCCGAGCGGAAGCTGTAACTGG 1740

ORIGIN		99.9%; Score 2178.8; DB 6; Length 2180;
Query Match		Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 TCGAGGCCAAGAAATTCGGACAGAGGCTTCGGGCAAGGCCCCCTTGAGAGCACTTGCTTCTT	60
DB	1 TCGAGGCCAAGAAATTCGGACAGAGGCTTCGGGCAAGGCCCCCTTGAGAGCACTTGCTTCTT	60
QY	61 TGGGCACTGTTGTGGAACAGGAGCAAGATGGACATGTACTTCTGGGAGATGGGTTTCCAAAT	120
DB	61 TGGGCACTGTTGTGGAACAGGAGCAAGATGGACATGTACTTCTGGGAGATGGGTTTCCAAAT	120
QY	121 GCATGTTCTCAGGCTCTTGAGGAGCTGTTTGTGCTCCGGATGATGCAAGCCCTGAGGCT	180
DB	121 GCATGTTCTCAGGCTCTTGAGGAGCTGTTTGTGCTCCGGATGATGCAAGCCCTGAGGCT	180
QY	181 GAGGCTGAGAGGAGCAAGCAAGGAGAAAGACTGGGCTTCAAGTTTGAAGGGATGGGCTT	240
DB	181 GAGGCTGAGAGGAGCAAGCAAGGAGAAAGACTGGGCTTCAAGTTTGAAGGGATGGGCTT	240
QY	241 GACCTCTTTGGGAGGTGCTATCGAGAGTGAAGGTGAAGGGCTGGCCGCTCTCTCCGT	300
DB	241 GACCTCTTTGGGAGGTGCTATCGAGAGTGAAGGTGAAGGGCTGGCCGCTCTCTCCGT	300
QY	301 CGCTGCCGCTCTGAGGAGATGCACTTGCCTCCAGCTGAGCAATGCAAGCTGACGCCCT	360
DB	301 CGCTGCCGCTCTGAGGAGATGCACTTGCCTCCAGCTGAGCAATGCAAGCTGACGCCCT	360
QY	361 GCTTTCTTTGGCCAGAGTGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATATG	420
DB	361 GCTTTCTTTGGCCAGAGTGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATATG	420
QY	421 GCGAGCACTACACCATCTGAGGCTTCTCGGCTTCTTTGGCCCTCACTGATCTAC	480
DB	421 GCGAGCACTACACCATCTGAGGCTTCTCGGCTTCTTTGGCCCTCACTGATCTAC	480
QY	481 ACCGCGCTCATCACCTTCAGAGAAATCAGAAAGAGAGCCCAACGAGAGAGACTGAGTTT	540
DB	481 ACCGCGCTCATCACCTTCAGAGAAATCAGAAAGAGAGCCCAACGAGAGAGACTGAGTTT	540
QY	541 GACATGATATGTATCTTAATAGGAGAAAGGCTGTCCGGAAGCGGAGCCAGCGAAG	600
DB	541 GACATGATATGTATCTTAATAGGAGAAAGGCTGTCCGGAAGCGGAGCCAGCGAAG	600
QY	601 ACGCGGCTGAGGAGGTCGCGGCGCAGTCCGAGGCTGTCGAGGAGCGGCTGCGG	660
DB	601 ACGCGGCTGAGGAGGTCGCGGCGCAGTCCGAGGCTGTCGAGGAGCGGCTGCGG	660
QY	661 GGGGCGGCTGCTACGCGCGCTGTTCCATTTGAGGCGGCGCGGATGCCATCTTCATG	720
DB	661 GGGGCGGCTGCTACGCGCGCTGTTCCATTTGAGGCGGCGCGGATGCCATCTTCATG	720
QY	721 GGGCACTGTGTACGTACTGTCTGTCTGCTTTTCTGCGGAGTGTCTGTGGAT	780
DB	721 GGGCACTGTGTACGTACTGTCTGTCTGCTTTTCTGCGGAGTGTCTGTGGAT	780
QY	781 TTTCCAGCGGCGGCGCGGCTCCCTGGAGCTGCTCTAATTTCTGGGCTTTTCAAGCTG	840
DB	781 TTTCCAGCGGCGGCGCGGCTCCCTGGAGCTGCTCTAATTTCTGGGCTTTTCAAGCTG	840
QY	841 CTGTGCGAGAACTGCGCAGAGGCTTGAGCGAGAGCGGAGCAAGCTTGCCAGCGGAGC	900
DB	841 CTGTGCGAGAACTGCGCAGAGGCTTGAGCGAGAGCGGAGCAAGCTTGCCAGCGGAGC	900
QY	901 CCGGCGGCTTGCGCATGTCTCACTAGCGAGCGCTGCGCTCTACCTGCGAGAGAGCTGG	960
DB	901 CCGGCGGCTTGCGCATGTCTCACTAGCGAGCGCTGCGCTCTACCTGCGAGAGAGCTGG	960
QY	961 AACCAATGCGACATAGTGGCTCTCAACCTGTTCTCCCTGAGGAGTGGCGGCTGACC	1020
DB	961 AACCAATGCGACATAGTGGCTCTCAACCTGTTCTCCCTGAGGAGTGGCGGCTGACC	1020

QY	1021 CCGGCTTGTACCACTGAGGCGGCACTGTCTCTGACATGCACTTCATGTGTTTACGAGTG	1080
DB	1021 CCGGCTTGTACCACTGAGGCGGCACTGTCTCTGACATGCACTTCATGTGTTTACGAGTG	1080
QY	1081 CCGTGTCTTCACTCTTCAAGGTCAACAAACAGTGGGAGCCCAAGATCTGATGTAGC	1140
DB	1081 CCGTGTCTTCACTCTTCAAGGTCAACAAACAGTGGGAGCCCAAGATCTGATGTAGC	1140
QY	1141 AAGATGATGAAGACGATGTTCTTCTCTCTTCTCTGCGGAGTGGAGTGGAGCTAT	1200
DB	1141 AAGATGATGAAGACGATGTTCTTCTCTCTTCTCTGCGGAGTGGAGTGGAGCTAT	1200
QY	1201 GCGGTGGCAACGAGAGGAGCTCTGAGGCAAGGAGAGTACCTTCCAAATGATCTGCGC	1260
DB	1201 GCGGTGGCAACGAGAGGAGCTCTGAGGCAAGGAGAGTACCTTCCAAATGATCTGCGC	1260
QY	1261 CGGCTCTTCAAGGCTCCCTCACTGAGAGATGTTGGGAGATTTCCCAAGAGAGACATGAGC	1320
DB	1261 CGGCTCTTCAAGGCTCCCTCACTGAGAGATGTTGGGAGATTTCCCAAGAGAGATGAGC	1320
QY	1321 GTGAGCTCATGAGAGCAAGCAACTGCTGTCGAGAGCCGAGCTTCTGGGCAACCTCTCT	1380
DB	1321 GTGAGCTCATGAGAGCAAGCAACTGCTGTCGAGAGCCGAGCTTCTGGGCAACCTCTCT	1380
QY	1381 GGGGCCAGGCGGAGCACCTGCTCTCCAGTATGCAATGAGTGGTGTGCTGCTCTC	1440
DB	1381 GGGGCCAGGCGGAGCACCTGCTCTCCAGTATGCAATGAGTGGTGTGCTGCTCTC	1440
QY	1441 GTCACTCTTCTGCTGAGGCAACATCTGCTGTCATCTTGTGCACTTGTGCACTTGTAGT	1500
DB	1441 GTCACTCTTCTGCTGAGGCAACATCTGCTGTCATCTTGTGCACTTGTGCACTTGTAGT	1500
QY	1501 TACACATTCGGCAAGTACAGGAGCAAGAGATCTACTGAAAGCGGAGGAGCTTACCGC	1560
DB	1501 TACACATTCGGCAAGTACAGGAGCAAGAGATCTACTGAAAGCGGAGGAGCTTACCGC	1560
QY	1561 CTCATCCGAGAAATTCACCTCTCGGCGCGCTGAGCCGCTTATGCTATCTCCAC	1620
DB	1561 CTCATCCGAGAAATTCACCTCTCGGCGCGCTGAGCCGCTTATGCTATCTCCAC	1620
QY	1621 TTTGGGCTCTGCTCAAGGCAATTTGTGAGGAGCAAGGAGAGCCCGAGCGGCTCTCCCG	1680
DB	1621 TTTGGGCTCTGCTCAAGGCAATTTGTGAGGAGCAAGGAGAGCCCGAGCGGCTCTCCCG	1680
QY	1681 GCCCTGAGCAATTCGAGGTTTACCTTTCTAAGAAAGCCGAGGAGAGTGTAAAGCTGG	1740
DB	1681 GCCCTGAGCAATTCGAGGTTTACCTTTCTAAGAAAGCCGAGGAGAGTGTAAAGCTGG	1740
QY	1741 GAAATCGGTGATTAAGAGAACTTTCTGTGCTGCAAGCGCTAGAGCAAGCGGAGAGCGAC	1800
DB	1741 GAAATCGGTGATTAAGAGAACTTTCTGTGCTGCAAGCGCTAGAGCAAGCGGAGAGCGAC	1800
QY	1801 TCCGAGGCTGAAAGCGGCAAGTCCGAAAGTGAAGTGTGCACTGAAACAGCTGGAGCAC	1860
DB	1801 TCCGAGGCTGAAAGCGGCAAGTCCGAAAGTGAAGTGTGCACTGAAACAGCTGGAGCAC	1860
QY	1861 ATCCGAGATGACAAAGCGCTGAAAGTCTGGAAGCGGAGGTTCCAGAGTGTACTCG	1920
DB	1861 ATCCGAGATGACAAAGCGCTGAAAGTCTGGAAGCGGAGGTTCCAGAGTGTACTCG	1920
QY	1921 GCCCGGCACTGTGTGCTTGTCTTGAAGTGAAGCCCATGTGCATCTGGGCACTGTC	1980
DB	1921 GCCCGGCACTGTGTGCTTGTCTTGAAGTGAAGCCCATGTGCATCTGGGCACTGTC	1980
QY	1981 AGGACCACTTTTGGAGTGTCACTTAAACAACAAGCATGCGGCTCTCCCAAGAC	2040
DB	1981 AGGACCACTTTTGGAGTGTCACTTAAACAACAAGCATGCGGCTCTCCCAAGAC	2040
QY	2041 CAGTCCAGGCTGGAGATCAAGGCTGAGTCCGAGGCGTTATCATCTGAGAGCTGC	2100
DB	2041 CAGTCCAGGCTGGAGATCAAGGCTGAGTCCGAGGCGTTATCATCTGAGAGGCTGC	2100